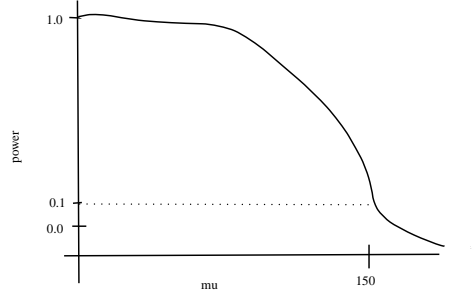
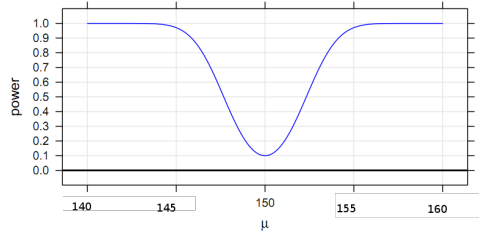


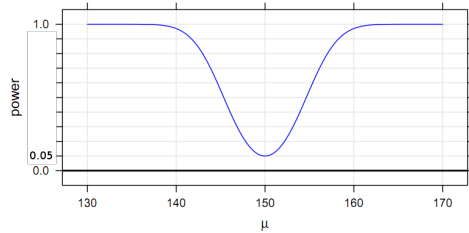
1. (a) Minimum is at 150.
- (b) Value at minimum is 0.10.
- (c) The minimum is in the middle of the graph, as opposed to being at one extreme.
- (d) 146, 154.
- (e) The minimum occurs as  $\mu \rightarrow \infty$  and is 0.1 at  $\mu = 150$ :



- (f) The curve is tighter around the minimum, i.e., there is more power because the sample size is bigger:



- (g) The value at minimum 0.05 instead of 0.10:



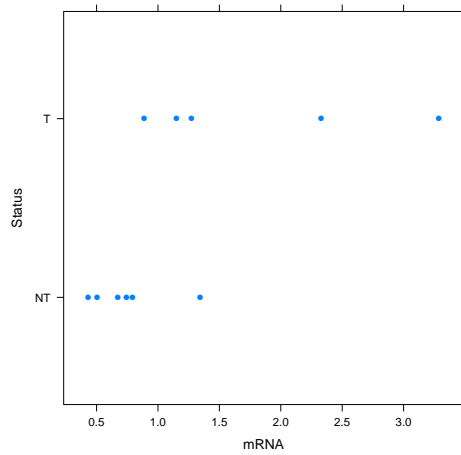
2. Please see attached sheets.

3. (a) 

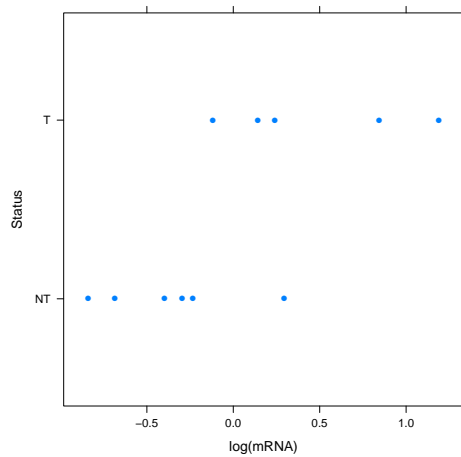
```
> c = read.csv("cichlids.csv")
> str(c)

'data.frame':      11 obs. of  2 variables:
 $ Status: Factor w/ 2 levels "NT","T": 1 1 1 1 1 1 2 2 2 2 ...
 $ mRNA  : num  0.504 0.432 0.744 0.792 0.672 ...

> plot(xyplot(Status~mRNA, data=c, pch=16))
```



(b) `> plot(xyplot(Status~log(mRNA), data=c, pch=16))`



(c) The second one shows less skewness.

(d) `> a = c[c$Status == "NT", "mRNA"]`  
`> b = c[c$Status == "T", "mRNA"]`  
`> o = t.test(a, b, paired=FALSE)`  
`> o$conf.int`

```
[1] -2.2631808 0.1879808
attr(,"conf.level")
[1] 0.95
```

(e) `> a = log(c[c$Status == "NT", "mRNA"])`  
`> b = log(c[c$Status == "T", "mRNA"])`  
`> o = t.test(a, b, paired=FALSE)`  
`> o$conf.int`

```
[1] -1.5019171 -0.1359423
attr(,"conf.level")
[1] 0.95
```